Certificate of Mailing under 37 CFR 1.8

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on ___February 8, 2002___ .
Date

Melissa McCullin
Signature

MELISSA MCCULLIN
Type or printed name of person signing Certificate

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09/665,308
BB11409 USNA
AMENDMENT
STATEMENT UNDER 37 CFR 1.821(g) AND 1.825(b)
SEQUENCE LISTING - CRF
SEQUENCE LISTING - 28 PAGES
RETURN RECEIPT CARD
COPIES OF ORIGINALS SENT ON OCT. 17, 2001: AMENDMENT, STATEMENT UNDER 37 CFR1.821(g) AND 1.825(b), CERTIFICATE OF MAIL DOCUMENT, AND RETURN RECEIPT CARD STAMPED BY THE USPTO
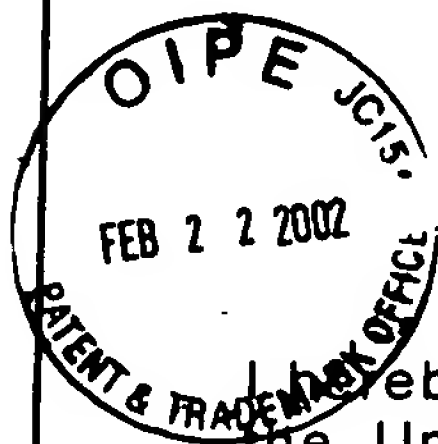
Certificate of Mailing under 37 CFR 1.8

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I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to:

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Melissa McCullin
Signature

MELISSA MCCULLIN
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09/665,308
BB1149 USNA
AMENDMENT
STATEMENT UNDER 37 CFR 1.821(g) AND 1.825(b)
SEQUENCE LISTING - CRF
SEQUENCE LISTING - 28 PAGES
Return Receipt Card MMc 11-13-01

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/665308	09/19/2000	CAHOON, REBECCA E.	BB1149 US NA

EXAMINER	
Cynthia Collins	
ART UNIT	PAPER NUMBER
1638	13

Please find below a communication from the EXAMINER in charge of this application

The communication filed July 23, 2001 is not fully responsive to the Office communication mailed June 18, 2001 for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the above-mentioned reply appears to be *bona fide* attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Cynthia Collins whose telephone number is (703) 605-1210. If the examiner cannot be reached, inquiries can be directed to Supervisory Patent Examiner Paula Hutzell whose telephone number is (703) 308-4310. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.
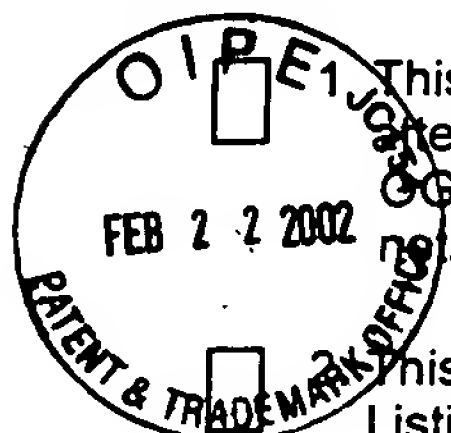
Cynthia Collins   October 12, 2001

ELIZABETH F. McELWAIN
PRIMARY EXAMINER
GROUP 1800

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of tim may b obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for th following reason(s):

1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequenc Listing" as required by 37 C.F.R. 1.821(c).

3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

[X] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

7. Other: _____

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Applicant Must Provide:

[X] An initial or <u>substitute</u> computer readable form (CRF) copy of the "Sequence Listing".

[X] An initial or <u>substitute</u> paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

[X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
    Technical Assistance...703-287-0200
    To Purchase PatentIn Software.......................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

COPY OF PAPERS ORIGINALLY FILED

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _C9/665,308A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

· 2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length .

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

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RAW SEQUENCE LISTING   DATE: 07/31/2001
PATENT APPLICATION: US/09/665,308A   TIME: 14:45:58

Input Set : A:\BB1149USNA Corrected Seq List.txt
Output Set: N:\CRF3\07312001\I665308A.raw

Does Not Comply
Corrected Diskette Needec

```
 3 <110> APPLICANT: Cahoon, Rebecca E.
 4         Klein, Theodore M.
 5         Odell, Joan T.
 6         Orozco, Emil M. Jr.
 8 <120> TITLE OF INVENTION: PLANT CELL CYCLIN GENES
.0 <130> FILE REFERENCE: BB1149 US NA
.2 <140> CURRENT APPLICATION NUMBER: US/09/665,308A
.2 <141> CURRENT FILING DATE: 2000-09-19
.2 <150> PRIOR APPLICATION NUMBER: 60/078,735
.3 <151> PRIOR FILING DATE: 1998 March 20    1998-03-20   use this date format
 5 <150> PRIOR APPLICATION NUMBER: PCT/US99/06047
 6 <151> PRIOR FILING DATE: 1999 March 19    1999-03-19
 8 <160> NUMBER OF SEQ ID NOS: 32
 0 <170> SOFTWARE: MICROSOFT OFFICE 97


 D SEQUENCES

)53 <210> SEQ ID NO: 21
)54 <211> LENGTH: 789
)55 <212> TYPE: DNA
:56 <213> ORGANISM: Triticum aestivum
:58 <400> SEQUENCE: 21
)59 cacctgaggg cgactcgagg gtgccctcgc cccgtccgcc gtgaccaccc ctcttcggat   60
.60 ctcaccgcct cgaccaaaat gtgatttgag gcaaattctg cgtttgaggc aaggacaata  120
:61 aaagtgatgg agcttttggt cttcagcacc ttgaaatgga ggatgcaagc tgttactgct  180
:62 tgctcgttta ttgactactt cctttgcaaa ttcaatgatc atgacacacc ctccatgctt  240
:63 gcattctcct gctcaactga cctcatcctg agcacaacta agtgagctga ttttttggtg  300
 64 ttcagacatt cagagattgc tggaagtgtt gcacttcctt catttgggga gcacaagact  360
 65 tcagttgtcg aaatggctac aactaattgc aagtatataa acaagggagt gtgatgtgac  420
 66 aggaaagatc ctgatgaagt gcttccttta tggaatgcct atctgaagtt tggactaaga  480
 67 gacatgcttt aattggctta gtaaaaaata cttgctaaag agaaataaga ttcaaagtag  540
 68 atgttttat tgtagattag gatatgtgtg ttctgccacc ggttcgactt ctcatattag  600
 69 aaggcaagca gttagttcat atcttactac tttgcactat tgtagatgga tggtgaggga  660
 70 ttgagaggct actactatta atgtgcgtaa actttgcatc tttagctctc taaatgaaac  720
 71 cggtgatggt taacctgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa  780
 72 aaaaaaaaa                                                      789 ← insert
 25 <210> SEQ ID NO: 23
 26 <211> LENGTH: 603  1132 (p.2)
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Zea mays
 30 <220> FEATURE:
 31 <221> NAME/KEY: unsure
 32 <222> LOCATION: (441)
 34 <220> FEATURE:
 35 <221> NAME/KEY: unsure
 36 <222> LOCATION: (447)
```

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1138 <220> FEATURE:
1139 <221> NAME/KEY: unsure
1140 <222> LOCATION: (485)
1142 <220> FEATURE:
1143 <221> NAME/KEY: unsure
1144 <222> LOCATION: (498)
1146 <220> FEATURE:
1147 <221> NAME/KEY: unsure
1148 <222> LOCATION: (528)
1150 <220> FEATURE:
1151 <221> NAME/KEY: unsure
1152 <222> LOCATION: (553)
1154 <220> FEATURE:
1155 <221> NAME/KEY: unsure
1156 <222> LOCATION: (560)
1158 <220> FEATURE:
1159 <221> NAME/KEY: unsure
1160 <222> LOCATION: (576)..(577)
1162 <220> FEATURE:
163 <221> NAME/KEY: unsure
164 <222> LOCATION: (598)
166 <400> SEQUENCE: 23
167 aacagaattc ggcacgagcc gcggtcggct gggtttcacg cgccgcggcg cggctaggct    60
168 tctccgcgct caccgccgcg ctcgccgccg cctacctcga ccgctgcttc ctccccgggg   120
169 gcgcgctccg gctcggcgac cagccctgga tggcgcgcct agccgccgtc acctgcttcg   180
170 cgctcgccgc caaggtcgag gagacgcgcg tgccgccgct cctcgacctc cagctctacg   240
171 ccgccgctga cgccgcggat ccgtacgtat tcgaggccaa gacggtgcgc cggatggagc   300
172 tgctcgtgct ctccgcgctt gggtggcgga tgcaccctgt cacgcccttc tcctacctcc   360
173 agcccgtcct cgccgacgct gcgacgcgcc tgcgtagctg cgagggcgtc ctgctcgcgg   420
174 tcatggccga ctggaggtgg cctcggcacc ggccttcggc gtgggccgcc gccgcgttgc   480
175 tgatcacagc cgccgccggc gacggcggcg acggcgacgg cgacacggag ctcctggcgc   540
176 tcatcaatgc ccccgaggac aagaccgccg agtgtgccaa gatcatctcc gaggtgacgg   600
177 gcatgagctt cctcgcctgc gatgtcggcg tgagcgccgg aaataagcgt aagcacgcgg   660
178 cggcgcagtt gtactcgccg ccgccgagcc cgagcggcgt gatcggcgcg ctgtcctgct   720
179 tcagctgcga gagctcgacg tccgccaccg ctatggctgc ggcggtcggc ccgtgggcgc   780
180 cgtcggcgtc cgtgtccgtg tcgtcctctc cagagccacc aggtcgggcc cccaagcgcg   840
181 cagcggcggc gtcggcgtcg gcgtcggcgt cagccggggt cgcgccaccg gtccaggtcc   900
182 cgcatcagct accccccgac gaggagagcc gcgacgcctg gccgtccacc tgcgccgcgt   960
183 gacgcaccgt gccggaaacg gtgcctatgg cgagaccgcc gttcggtggc ggtggagaat  1020
184 ggagaacaag gagcatcatt ggctcgcgtc ggtgagcagg agaacgaact attttgccca  1080
185 ttgccgtgac agatggggggg tgttcactgc gtggagccgc gctgaⓐcaat ga         1132
106 <210> SEQ ID NO: 32
107 <211> LENGTH: 373
108 <212> TYPE: PRT
109 <213> ORGANISM: Nicotiana tabacum
111 <400> SEQUENCE: 32
112 Met Ala Ile Glu His Asn Glu Gln Gln Glu Leu Ser Gln Ser Phe Leu
113   1               5                  10                  15
115 Leu Asp Ala Leu Tyr Cys Glu Glu Glu Glu Glu Lys Trp Gly Asp Leu
```

see item 9 on Erra Summary Sheet

P.3

RAW SEQUENCE LISTING   DATE: 07/31/2001
PATENT APPLICATION: US/09/665,308A   TIME: 14:45:58

Input Set : A:\BB1149USNA Corrected S q List.txt
Output Set: N:\CRF3\07312001\I665308A.raw

```
1616                20                        25                        30
1618 Val Asp Asp Glu Thr Ile Ile Thr Pro Leu Ser Ser Glu Val Thr Thr
1619            35                        40                        45
1621 Thr Thr Thr Thr Thr Thr Lys Pro Asn Ser Leu Leu Pro Leu Leu Leu
1622       50                        55                        60
1624 Leu Glu Gln Asp Leu Phe Trp Glu Asp Glu Glu Leu Leu Ser Leu Phe
1625 65                        70                        75                  80
1627 Ser Lys Glu Lys Glu Thr His Cys Trp Phe Asn Ser Phe Gln Asp Asp
1628                      85                        90                        95
1630 Ser Leu Leu Cys Ser Ala Arg Val Asp Ser Val Glu Trp Ile Leu Lys
1631            100                       105                       110
1633 Val Asn Gly Tyr Tyr Gly Phe Ser Ala Leu Thr Ala Val Leu Ala Ile
1634            115                       120                       125
1636 Asn Tyr Phe Asp Arg Phe Leu Thr Ser Leu His Tyr Gln Lys Asp Lys
1637       130                       135                       140
1639 Pro Trp Met Ile Gln Leu Ala Ala Val Thr Cys Leu Ser Leu Ala Ala
1640 145                       150                       155                 160
1642 Lys Val Glu Glu Thr Gln Val Pro Leu Leu Leu Asp Phe Gln Val Glu
1643            165                       170                       175
1645 Asp Ala Lys Tyr Val Phe Glu Ala Lys Thr Ile Gln Arg Met Glu Leu
1646            180                       185                       190
1648 Leu Val Leu Ser Ser Leu Lys Trp Arg Met Asn Pro Val Thr Pro Leu
1649       195                       200                       205
1651 Ser Phe Leu Asp His Ile Ile Arg Arg Leu Gly Leu Arg Asn Asn Ile
1652       210                       215                       220
1654 His Trp Glu Phe Leu Arg Arg Cys Glu Asn Leu Leu Leu Ser Ile Met
1655 225                       230                       235                 240
1657 Ala Asp Cys Arg Phe Val Arg Tyr Met Pro Ser Val Leu Ala Thr Ala
1658            245                       250                       255
1660 Ile Met Leu His Val Ile His Gln Val Glu Pro Cys Asn Ser Val Asp
1661            260                       265                       270
1663 Tyr Gln Asn Gln Leu Leu Gly Val Leu Lys Ile Asn Lys Glu Lys Val
1664       275                       280                       285
1666 Asn Asn Cys Phe Glu Leu Ile Ser Glu Val Cys Ser Lys Pro Ile Ser
1667       290                       295                       300
1669 His Lys Arg Lys Tyr Glu Asn Pro Ser His Ser Pro Ser Gly Val Ile
1670 305                       310                       315                 320
1672 Asp Pro Ile Tyr Ser Ser Glu Ser Ser Asn Asp Ser Trp Asp Leu Glu
1673            325                       330                       335
1675 Ser Thr Ser Ser Tyr Phe Pro Val Phe Lys Lys Ser Arg Val Gln Glu
1676            340                       345                       350
1678 Gln Gln Met Lys Leu Ala Ser Ser Ile Ser Arg Val Phe Val Glu Ala
1679            355                       360                       365
1681 Val Gly Ser Pro His
1682       370
1685 (6)
```

delete

→ Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding ...
... in the <223> to <226> fields of
each sequence using n or Xaa.

Input Set : A:\BB1149USNA Corrected Seq List.txt
Output Set: N:\CRF3\07312001\I665308A.raw

M:270 C: Current Application Number differs, Replaced Current Application No
M:271 C: Current Filing Date differs, Replaced Current Filing Date
M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/665,308A

DATE: 07/31/2001
TIME: 14:45:59

Input Set : A:\BB1149USNA Corrected Seq List.txt
Output Set: N:\CRP3\07312001\I665308A.raw

M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:20
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:789 SEQ:21
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
M:252 E: No. of Seq. differs, <211>LENGTH:Input:603 Found:1132 SEQ:23
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32

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